

AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A promoter DNA recognized by SigA and SigE, which is produced by modifying a nucleotide sequence including a promoter recognized by SigA and bases in the vicinity thereof,

wherein the consensus sequence recognized by SigE is a nucleotide sequence comprising a -35 region represented by ATAHTT and a -10 region represented by CATAYAHT, which is linked to a site 13 or 14 nucleotides downstream from the -35 region, wherein H denotes A, C, or T and Y denotes C or T, and

wherein the consensus sequence recognized by SigA is a nucleotide sequence comprising a -35 region represented by TTGACA and a -10 region represented by TGNTATAAT, which is linked to a site 14 nucleotides downstream from the -35 region, wherein N represents A, G, C, or T.

2. - 3. (Canceled)

4. (Currently Amended) ~~The promoter DNA as described in any one of claims 1 to 3~~  
A promoter DNA recognized by SigA and SigE, which is produced by modifying a nucleotide sequence including a promoter recognized by SigA and bases in the vicinity thereof, to be further recognized by SigE, with the promoter recognized by SigA being maintained,

wherein the consensus sequence recognized by SigE is a nucleotide sequence comprising a -35 region represented by ATAHTT and a -10 region represented by CATAYAHT, wherein H denotes A, C, or T and Y denotes C or T, which is linked to a site 13 or 14 nucleotides downstream from the -35 region, and

wherein the nucleotide sequence including a promoter recognized by SigA and bases in the vicinity thereof comprises a nucleotide sequence ranging from base Nos. 92 to 552 in SEQ ID NO: 1, a nucleotide sequence ranging from base Nos. 133 to 589 in SEQ ID NO: 2, or a nucleotide sequence having a homology of 80% or more to either of these nucleotide sequences and having a the consensus sequence of recognized by SigA and/or promoter functions equivalent to those of the consensus sequence.

5. (Currently Amended) The promoter DNA according to claim 4 as described in any of claims 1 to 3, wherein the nucleotide sequence including a promoter recognized by SigA and bases in the vicinity thereof comprises a nucleotide sequence represented by ranging from base Nos. 92 to 552 in SEQ ID NO: 1, a nucleotide sequence represented by ranging from base Nos. 133 to 589 in SEQ ID NO: 2, or a nucleotide sequence having a homology of 90% or more to either of these nucleotide sequences and having a the consensus sequence recognized by SigA and/or promoter functions equivalent to those of the consensus sequence.

6. (Currently Amended) The promoter DNA according to claim 4 as described in claim 4 or 5, wherein the nucleotide sequence having a promoter recognized by SigA and bases in the vicinity of the promoter has a size of 610 bp or less.

7. (Currently Amended) A promoter DNA which is produced by ligating two or more promoter DNAs according to claim 1 as described in any one of claims 1 to 6.

8. (Currently Amended) An expression vector which has the promoter DNA according to claim 1 as described in any one of claims 1 to 7.

9. (Currently Amended) A recombinant microorganism which has the expression vector ~~as described in~~ according to claim 8.

10. (Currently Amended) A recombinant microorganism which has the promoter DNA ~~according to claim 1 as described in any one of claims 1 to 7~~ on the genome.

11. (Currently Amended) A method for producing a protein or a polypeptide, characterized by comprising culturing the recombinant microorganism according to claim 9 ~~as described in claim 9 or 10~~.

12. (Currently Amended) The method ~~as described in~~ according to claim 11, wherein the protein is cellulase or amylase.

13. (Currently Amended) The method ~~as described in~~ according to claim 12, wherein the cellulase is an alkaline cellulase which has an amino acid sequence of SEQ ID NO: 4, or a protein which has a homology of 70% or more to the amino acid sequence and alkaline cellulase activity.

14. (Currently Amended) The method ~~as described in~~ according to claim 12, wherein the amylase is an alkaline amylase which has an amino acid sequence of SEQ ID NO: 14, or a protein which has a homology of 70% or more to the amino acid sequence and alkaline amylase activity.

15. (Currently Amended) A method for constructing a promoter DNA, characterized by comprising modifying a nucleotide sequence having a promoter recognized by SigA and having a nucleotide present in the vicinity of the promoter so as to be recognized by SigA and SigE, wherein said promoter DNA is a promoter DNA according to claim 1.

16. (New) A method for producing a protein or a polypeptide, comprising culturing the recombinant microorganism according to claim 10.

17. (New) The method according to claim 16, wherein the protein is cellulase or amylase.

18. (New) The method according to claim 17, wherein the cellulase is an alkaline cellulase which has an amino acid sequence of SEQ ID NO: 4, or a protein which has a homology of 70% or more to the amino acid sequence and alkaline cellulase activity.

19. (New) The method according to claim 17, wherein the amylase is an alkaline amylase which has an amino acid sequence of SEQ ID NO: 14, or a protein which has a homology of 70% or more to the amino acid sequence and alkaline amylase activity.

20. (New) The promoter DNA according to claim 1, wherein the consensus sequence recognized by SigE is a nucleotide sequence comprising a -35 region represented by ATATTT and a -10 region represented by CATAACAAT which is linked to a site 13 or 14 nucleotides downstream from the -35 region.

21. (New) The promoter DNA according to claim 1, wherein the consensus sequence recognized by SigE is a nucleotide sequence represented by  
ATATTCAAGTAGTAATAACATACAAT.

22. (New) The promoter DNA according to claim 1, wherein said promoter DNA comprises the nucleotide sequence of SEQ ID NO: 7.

23. (New) The promoter DNA according to claim 1, wherein said promoter DNA comprises the nucleotide sequence of SEQ ID NO: 8.